AMENDMENTS

In the Claims:

Please cancel claims 88-104 and 106-114 without prejudice. Please add new claims 162 to 182. Please amend claims 115-127, 138, 144, and 154-161 to read as follows. The pending claims are as follows.

G1 Sub 172

115. (Amended once) A method of selecting biological samples from human individuals, said method comprising selecting from a supply of human biological samples, samples that contain a detectable polynucleotide comprising a contiguous sequence of at least 15 nucleotides fully complementary to either strand of Figure 3.

116. (Amended once) A method of selecting biological samples from human individuals, said method comprising selecting from a supply of human biological samples, biological samples that contain a detectable polynucleotide comprising a contiguous sequence of at least 15 nucleotides fully complementary to either strand of Figure 62A.

117. (Amended once) A method of selecting biological samples from human individuals, said method comprising selecting from a supply of human biological samples, biological samples that contain a detectable polynucleotide comprising a contiguous sequence of at least 15 nucleotides fully complementary to either strand of Figure 89.

G2 Sub 173

118. (Amended once) A method of selecting biological samples from human individuals, said method comprising selecting from a supply of human biological samples, samples that comprise either (i) a polynucleotide that hybridizes under stringent conditions to a polynucleotide that comprises a contiguous sequence of at least 15 nucleotides from the genome

of a hepatitis C virus genome or the complement thereof, or (ii) antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by a hepatitis C virus genome.

119. (Amended once) A method of selecting biological samples from human individuals, said method comprising selecting from a supply of human biological samples, samples that comprise either (i) a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides from either strand of at least one of the HCV cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394 or (ii) antibodies that form an antigen-antibody complex with an HCV polypeptide sequence of at least 10 contiguous amino acid encoded by an HCV cDNA insert in the lambda gt-11 library deposited as ATCC deposit No. 40394.

120. (Amended once) A method of selecting biological samples from human individuals comprising selecting from a supply of human biological samples, samples that comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides found in either strand of Figure 89.

121. (Amended once) A method of selecting biological samples from human individuals comprising selecting from a supply of human biological samples, samples that comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides found in either strand of Figure 14.

G2

122. (Amended once) A method of selecting biological samples from human individuals comprising selecting from a supply of human biological samples, samples that comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15

nucleotides from either strand of at least one of the hepatitis C virus (HCV) cDNA inserts in [the] a lambda gt-11 cDNA library deposited as ATCC No. 40394.

123. (Amended once) A method of selecting biological samples from human individuals comprising selecting from a supply of human biological samples, samples that comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 90.

124. (Amended once) A method of selecting biological samples from human individuals comprising selecting from a supply of human biological samples, samples that comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 14.

125. (Amended once) A method of selecting biological samples from human individuals comprising selecting from a supply of human biological samples, samples that comprise antibodies that form an antigen-antibody complex with a hepatitis C virus (HCV) polypeptide sequence of at least 10 contiguous amino acid encoded by an HCV cDNA insert in [the] a lambda gt-11 library deposited as ATCC deposit No. 40394.

126. (Amended once) A method according to any of claims 118-122 wherein said stringent conditions permit the formation of a stable hybrid duplex between said polynucleotide and said contiguous sequence and do not permit the formation of a stable duplex between said contiguous sequence and the genomes of Hepatitis B or Hepatitis A viruses.

62 127. (Amended once) A method according to any of claims 115-122, 162 or 163 wherein said polynucleotide is detectable in a PCR assay.

128. A method according to claim 126 wherein said polynucleotide is detectable in a PCR assay.

129. A method according to any of claims 118, 119, and 123-125 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

130. A method according to claim 129 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

131. A method according to claim 130 wherein said antigen is a fusion protein.

132. A method according to any of claims 115-125, 162 or 163 wherein said biological samples are blood .

133. A method according to claim 126 wherein said biological samples are blood.

134. A method according to claim 127 wherein said biological samples are blood.

135. A method according to claim 128 wherein said biological samples are blood.

136. A method according to claim 129 wherein said biological samples are blood.

137. A method according to claim 130 wherein said biological samples are blood.

C3 SUB A3 138. (Amended once) A method according to any of claims 115-125, 162 or 163 wherein said biological samples are plasma.

139. A method according to claim 126 wherein said biological samples are plasma.

140. A method according to claim 127 wherein said biological samples are plasma.

141. A method according to claim 128 wherein said biological samples are plasma.

142. A method according to claim 129 wherein said biological samples are plasma.

143. A method according to claim 130 wherein said biological samples are plasma.

C4 SUB A4 144. (Amended once) A method according to any of claims 115-125, 162 or 163 wherein said biological samples are sera.

145. A method according to claim 126 wherein said biological samples are sera.

146. A method according to claim 127 wherein said biological samples are sera.

147. A method according to claim 128 wherein said biological samples are sera.

148. A method according to claim 129 wherein said biological samples are sera.

149. A method according to claim 130 wherein said biological samples are sera.

150. A method according to claim 132 further comprising employing biological samples that are not selected for a preparation of blood-related products.

151. A method according to claim 133 further comprising employing biological samples that are not selected for a preparation of blood-related products.

152. A method according to claim 138 further comprising employing biological samples that are not selected for a preparation of blood-related products.

153. A method according to claim 139 further comprising employing biological samples that are not selected for a preparation of blood-related products.

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154. (Amended once) A method according to claim 132 wherein said selected samples are for use in passive immunotherapy.

155. (Amended once) A method according to claim 133 wherein said selected samples are for use in passive immunotherapy.

156. (Amended once) A method according to claim 138 wherein said selected samples are for use in passive immunotherapy.

157. (Amended once) A method according to claim 142 wherein said selected samples are for use in passive immunotherapy.

158. (Amended once) A method according to claim 132 wherein said samples are for use in the preparation of polyclonal antibodies.

159. (Amended once) A method according to claim 133 wherein said samples are for use in the preparation of polyclonal antibodies.

160. (Amended once) A method according to claim 138 wherein said samples are for use in the preparation of polyclonal antibodies.

161. (Amended once) A method according to claim 142 wherein said samples are for use in the preparation of polyclonal antibodies.

162. (New) A method of selecting biological samples from human individuals, said method comprising selecting from a supply of human biological samples, samples that contain a detectable polynucleotide comprising a sequence that is fully complementary to a contiguous sequence of at least 15 nucleotides from the genome of a hepatitis C virus genome or the complement thereof.

163. (New) A method of selecting biological samples from human individuals, said method comprising selecting from a supply of human biological samples, samples that contain a detectable polynucleotide comprising a sequence that is fully complementary to a contiguous sequence of at least 15 nucleotides from either strand of at least one of the HCV cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.

164. (New) A method according to claim 132 wherein the selecting is to identify an HCV positive sample for removal from the supply.

165. (New) A method according to claim 133 wherein the selecting is to identify an HCV positive sample for removal from the supply.

166. (New) A method according to claim 134 wherein the selecting is to identify an HCV positive sample for removal from the supply.

167. (New) A method according to claim 144 further comprising employing biological samples that are not selected for a preparation of blood-related products.

168. (New) A method according to claim 135 wherein the selecting is to identify an HCV positive sample for removal from the supply.

169. (New) A method according to claim 136 wherein the selecting is to identify an HCV positive sample for removal from the supply.

170. (New) A method according to claim 137 wherein the selecting is to identify an HCV positive sample for removal from the supply.

171. (New) A method according to claim 138 wherein the selecting is to identify an HCV positive sample for removal from the supply.

172. (New) A method according to claim 139 wherein the selecting is to identify an HCV positive sample for removal from the supply.

173. (New) A method according to claim 140 wherein the selecting is to identify an HCV positive sample for removal from the supply.

174. (New) A method according to claim 141 wherein the selecting is to identify an HCV positive sample for removal from the supply.

175. (New) A method according to claim 142 wherein the selecting is to identify an HCV positive sample for removal from the supply.

176. (New) A method according to claim 143 wherein the selecting is to identify an HCV positive sample for removal from the supply.

177. (New) A method according to claim 144 wherein the selecting is to identify an HCV positive sample for removal from the supply.

178. (New) A method according to claim 145 wherein the selecting is to identify an HCV positive sample for removal from the supply.

179. (New) A method according to claim 146 wherein the selecting is to identify an HCV positive sample for removal from the supply.

180. (New) A method according to claim 147 wherein the selecting is to identify an HCV positive sample for removal from the supply.

181. (New) A method according to claim 148 wherein the selecting is to identify an HCV positive sample for removal from the supply.